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RAW SEQUENCE LISTING

DATE: 12/21/2001

PATENT APPLICATION: US/09/897,322

TIME: 15:03:37

Input Set : N:\Crf3\RULE60\09897322.txt

Output Set: N:\CRF3\12212001\I897322.raw

9 <110> APPLICANT: Valenzuela et al.
 13 <120> TITLE OF INVENTION: DORSAL TISSUE AFFECTING FACTOR AND COMPOSITIONS
 17 <130> FILE REFERENCE: REG132-B
 19 <140> CURRENT APPLICATION NUMBER: 09/897,322
 21 <141> CURRENT FILING DATE: 2001-07-02
 24 <150> PRIOR APPLICATION NUMBER: 09/167,874
 26 <151> PRIOR FILING DATE: 1998-10-07
 30 <150> PRIOR APPLICATION NUMBER: 08/485,721
 32 <151> PRIOR FILING DATE: 1995-07-06
 36 <150> PRIOR APPLICATION NUMBER: 08/392,935
 38 <151> PRIOR FILING DATE: 1995-09-22
 42 <150> PRIOR APPLICATION NUMBER: PCT/US93/08326
 44 <151> PRIOR FILING DATE: 1993-09-02
 48 <150> PRIOR APPLICATION NUMBER: 07/957,401
 50 <151> PRIOR FILING DATE: 1992-10-06
 54 <150> PRIOR APPLICATION NUMBER: 07/950,410
 56 <151> PRIOR FILING DATE: 1992-09-23
 60 <150> PRIOR APPLICATION NUMBER: 07/939,954
 62 <151> PRIOR FILING DATE: 1992-09-03
 66 <160> NUMBER OF SEQ ID NOS: 22
 70 <170> SOFTWARE: PatentIn Ver. 2.0
 74 <210> SEQ ID NO: 1
 76 <211> LENGTH: 699
 78 <212> TYPE: DNA
 80 <213> ORGANISM: Homo sapiens
 84 <220> FEATURE:
 86 <221> NAME/KEY: CDS
 88 <222> LOCATION: (1)..(696)
 92 <400> SEQUENCE: 1
 94 atg gag cgc tgc ccc agc cta ggg gtc acc ctc tac gcc ctg gtg gtg 48
 96 Met Glu Arg Cys Pro Ser Leu Gly Val Thr Leu Tyr Ala Leu Val Val
 98 1 5 10 15
 102 gtc ctg ggg ctg cgg gcg aca ccg gcc ggc ggc cag cac tat ctc cac 96
 104 Val Leu Gly Leu Arg Ala Thr Pro Ala Gly Gly Gln His Tyr Leu His
 106 20 25 30
 110 atc cgc ccg gca ccc agc gac aac ctg ccc ctg gtg gac ctc atc gaa 144
 112 Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
 114 35 40 45
 118 cac cca gac cct atc ttt gac ccc aag gaa aag gat ctg aac gag acg 192
 120 His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
 122 50 55 60
 126 ctg ctg cgc tgc ctg ctc ggg ggc cac tac gac cca ggc ttc atg gcc 240
 128 Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
 130 65 70 75 80
 134 acc tcg ccc ccc gag gac cgg ccc ggc ggg ggc ggg ggt gca gct ggg 288
 136 Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Gly Ala Ala Gly
 138 85 90 95

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142 ggc gcg gag gac ctg gcg gag ctg gac cag ctg ctg cgg cag cgg ccg 336
144 Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
146      100      105      110
150 tcg ggg gcc atg ccg agc gag atc aaa ggg cta gag ttc tcc gag ggc 384
152 Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
154      115      120      125
158 ttg gcc cag ggc aag aag cag cgc cta agc aag aag ctg cgg agg aag 432
160 Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
162      130      135      140
166 tta cag atg tgg ctg tgg tcg cag aca ttc tgc ccc gtg ctg tac gcg 480
168 Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala
170 145      150      155      160
174 tgg aac gac ctg ggc agc cgc ttt tgg ccg cgc tac gtg aag gtg ggc 528
176 Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
178      165      170      175
182 agc tgc ttc agt aag cgc tcg tgc tcc gtg ccc gag ggc atg gtg tgc 576
184 Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys
186      180      185      190
190 aag ccg tcc aag tcc gtg cac ctc acg gtg ctg cgg tgg cgc tgt cag 624
192 Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
194      195      200      205
198 cgg cgc ggg ggc cag cgc tgc ggc tgg att ccc atc cag tac ccc atc 672
200 Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
202      210      215      220
206 att tcc gag tgc aag tgc tcg tgc tag 699
208 Ile Ser Glu Cys Lys Cys Ser Cys
210 225      230
216 <210> SEQ ID NO: 2
218 <211> LENGTH: 232
220 <212> TYPE: PRT
222 <213> ORGANISM: Homo sapiens
226 <400> SEQUENCE: 2
228 Met Glu Arg Cys Pro Ser Leu Gly Val Thr Leu Tyr Ala Leu Val Val
230 1      5      10      15
234 Val Leu Gly Leu Arg Ala Thr Pro Ala Gly Gly Gln His Tyr Leu His
236      20      25      30
240 Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
242      35      40      45
246 His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
248      50      55      60
252 Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
254 65      70      75      80
258 Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Gly Ala Ala Gly
260      85      90      95
264 Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
266      100      105      110
270 Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
272      115      120      125
276 Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys

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278      130      135      140
282 Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala
284 145      150      155      160
288 Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
290      165      170      175
294 Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys
296      180      185      190
300 Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
302      195      200      205
306 Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
308      210      215      220
312 Ile Ser Glu Cys Lys Cys Ser Cys
314 225      230
320 <210> SEQ ID NO: 3
322 <211> LENGTH: 14
324 <212> TYPE: PRT
326 <213> ORGANISM: frog and mouse
330 <400> SEQUENCE: 3
332 Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr
334 1      5      10
340 <210> SEQ ID NO: 4
342 <211> LENGTH: 12
344 <212> TYPE: PRT
346 <213> ORGANISM: frog and mouse
350 <400> SEQUENCE: 4
352 Arg Phe Trp Pro Arg Tyr Val Lys Val Gly Ser Cys
354 1      5      10
360 <210> SEQ ID NO: 5
362 <211> LENGTH: 14
364 <212> TYPE: PRT
366 <213> ORGANISM: frog and mouse
370 <400> SEQUENCE: 5
372 Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys Lys
374 1      5      10
380 <210> SEQ ID NO: 6
382 <211> LENGTH: 8
384 <212> TYPE: PRT
386 <213> ORGANISM: frog and mouse
390 <400> SEQUENCE: 6
392 Leu Arg Trp Arg Cys Gln Arg Arg
394 1      5
400 <210> SEQ ID NO: 7
402 <211> LENGTH: 8
404 <212> TYPE: PRT
406 <213> ORGANISM: frog and mouse
410 <400> SEQUENCE: 7
412 Ile Ser Glu Cys Lys Cys Ser Cys
414 1      5
420 <210> SEQ ID NO: 8

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Input Set : N:\Crf3\RULE60\09897322.txt

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422 <211> LENGTH: 36
424 <212> TYPE: DNA
426 <213> ORGANISM: Artificial Sequence
430 <220> FEATURE:
432 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
436 <400> SEQUENCE: 8
438 gactcgagtc gacatcgag atgtggctgt ggtcac 36
444 <210> SEQ ID NO: 9
446 <211> LENGTH: 37
448 <212> TYPE: DNA
450 <213> ORGANISM: Artificial Sequence
454 <220> FEATURE:
456 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
460 <400> SEQUENCE: 9
462 ccaagcttct agaattcgca ggaacactta cactcgg 37
468 <210> SEQ ID NO: 10
470 <211> LENGTH: 1180
472 <212> TYPE: DNA
474 <213> ORGANISM: mouse
478 <220> FEATURE:
480 <221> NAME/KEY: CDS
482 <222> LOCATION: (421)..(1116)
486 <220> FEATURE:
488 <221> NAME/KEY: modified_base
490 <222> LOCATION: (16)
492 <223> OTHER INFORMATION: n=a, c, g, or t
496 <220> FEATURE:
498 <221> NAME/KEY: modified_base
500 <222> LOCATION: (235)
502 <223> OTHER INFORMATION: n=a, c, g, or t
506 <400> SEQUENCE: 10
W--> 508 taactcactc attagnaccc ccagccttac actttatgct tccggctcgt atgttgtgtg 60
512 gaattgtgag cggataacaa tttcacacag gaaacagcta tgaccatgat tacgccaagc 120
516 tcgaaattaa cctcactaa agggaacaaa agctggagct ccaccgcgtt ggcggccgcc 180
W--> 520 ttcccaagta gagcggcggg ggggaattgc gaccaactcg tgcgcgtctt ctgcncgcgc 240
524 ggcggagccg gcgctgcgcg aacggctctc ctgcagctc atgctgcctg cctgcgcct 300
528 gctcagcctc gggtagcca cctccggagg gaccggggag cgcggcagcg ccgcggactc 360
532 ggcgtgctct cctccgggga cgcgggacga agaggcagcc ccggggcgcg cgcgggaggc 420
536 atg gag cgc tgc ccc agc ctg ggg gtc acc ctc tac gcc ctg gtg gtg 468
538 Met Glu Arg Cys Pro Ser Leu Gly Val Thr Leu Tyr Ala Leu Val Val
540 1 5 10 15
544 gtc ctg ggg ctg cgg gca gca cca gcc ggc ggc cag cac tat cta cac 516
546 Val Leu Gly Leu Arg Ala Ala Pro Ala Gly Gly Gln His Tyr Leu His
548 20 25 30
552 atc cgc cca gca ccc agc gac aac ctg ccc ttg gtg gac ctc atc gaa 564
554 Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
556 35 40 45
560 cat cca gac cct atc ttt gac cct aag gag aag gat ctg aac gag acg 612
562 His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr

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564      50      55      60
568 ctg ctg cgc tcg ctg ctc ggg ggc cac tac gac ccg ggc ttt atg gcc 660
570 Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
572 65      70      75      80
576 act tcg ccc cca gag gac cga ccc gga ggg ggc ggg gga ccg gct gga 708
578 Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Gly Pro Ala Gly
580      85      90      95
584 ggt gcc gag gac ctg gcg gag ctg gac cag ctg ctg cgg cag cgg ccg 756
586 Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
588      100      105      110
592 tcg ggg gcc atg ccg agc gag atc aaa ggg ctg gag ttc tcc gag ggc 804
594 Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
596      115      120      125
600 ttg gcc caa ggc aag aaa cag cgc ctg agc aag aag ctg agg agg aag 852
602 Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
604      130      135      140
608 tta cag atg tgg ctg tgg tca cag acc ttc tgc ccg gtg ctg tac gcg 900
610 Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala
612 145      150      155      160
616 tgg aat gac cta ggc agc cgc ttt tgg cca cgc tac gtg aag gtg ggc 948
618 Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
620      165      170      175
624 agc tgc ttc agc aag cgc tcc tgc tct gtg ccc gag ggc atg gtg tgt 996
626 Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys
628      180      185      190
632 aag cca tcc aag tct gtg cac ctc acg gtg ctg cgg tgg cgc tgt cag 1044
634 Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
636      195      200      205
640 cgg cgc ggg ggt cag cgc tgc ggc tgg att ccc atc cag tac ccc atc 1092
642 Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
644      210      215      220
648 att tcc gag tgt aag tgt tcc tgc tagaactcgg gggggggcccc tgccccgcgcc 1146
650 Ile Ser Glu Cys Lys Cys Ser Cys
652 225      230
656 cagacacttg atggatcccc cgggctgaga tttt 1180
662 <210> SEQ ID NO: 11
664 <211> LENGTH: 232
666 <212> TYPE: PRT
668 <213> ORGANISM: mouse
672 <400> SEQUENCE: 11
674 Met Glu Arg Cys Pro Ser Leu Gly Val Thr Leu Tyr Ala Leu Val Val
676 1      5      10      15
680 Val Leu Gly Leu Arg Ala Ala Pro Ala Gly Gly Gln His Tyr Leu His
682      20      25      30
686 Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
688      35      40      45
692 His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
694      50      55      60
698 Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09897322.txt

Output Set: N:\CRF3\12212001\I897322.raw

L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:814 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:878 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:932 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:966 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1020 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22